



## **RAW SEQUENCE LISTING** **ERROR REPORT**

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Application Serial Number: 09/641,319B  
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PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

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2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P O. Box 2327, Arlington, VA 22202
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Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
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Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202



OIPE

Does Not Comply  
Correction Suggested Needed

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/641,319B

DATE: 04/26/2002

TIME: 12:39:38

Input Set : A:\04578--1.txt

Output Set: N:\CRF3\04262002\I641319B.raw

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3 <110> APPLICANT: Slater, Michael
4   Huang, Fen
5   Hartnett, James
7 <120> TITLE OF INVENTION: Mutant TNE Polymerases
9 <130> FILE REFERENCE: PRMG-04578
11 <140> CURRENT APPLICATION NUMBER: 09/641,319B
12 <141> CURRENT FILING DATE: 2000-08-18
14 <150> PRIOR APPLICATION NUMBER: 09/385,986
15 <151> PRIOR FILING DATE: 1999-08-30
17 <150> PRIOR APPLICATION NUMBER: 08/484,661
18 <151> PRIOR FILING DATE: 1995-06-07
20 <160> NUMBER OF SEQ ID NOS: 51
22 <170> SOFTWARE: PatentIn version 3.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2682
26 <212> TYPE: DNA
27 <213> ORGANISM: Thermotoga neapolitana
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31 <222> LOCATION: (1)..(2679)
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36 1          5          10          15
38 tat tac gcc ctc gac aga tcc ctt tcc aca tcc aca gga att cca acg      96
39 Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr
40          20          25          30
42 aac gcc gtc tat ggc gtt gcc agg atg ctc gtt aaa ttc ata aag gaa      144
43 Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu
44          35          40          45
46 cac att ata ccc gaa aag gac tac gcg gct gtg gcc ttc gac aag aag      192
47 His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys
48          50          55          60
50 gca gcg acg ttc aga cac aaa ctg ctc gaa gcg tac aag gcg caa agg      240
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56          85          90          95
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60          100          105          110
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64			115					120					125				
66	gat	gag	att	ttc	ata	ata	acc	ggt	gac	aag	gat	atg	ctt	caa	ctt	gta	432
67	Asp	Glu	Ile	Phe	Ile	Ile	Thr	Gly	Asp	Lys	Asp	Met	Leu	Gln	Leu	Val	
68		130					135					140					
70	aac	gag	aag	ata	aag	gtc	tgg	aga	atc	gtc	aag	ggg	ata	tcg	gat	ctt	480
71	Asn	Glu	Lys	Ile	Lys	Val	Trp	Arg	Ile	Val	Lys	Gly	Ile	Ser	Asp	Ileu	
72	145					150				155					160		
74	gag	ctt	tac	gat	tcg	aaa	aag	gtg	aaa	gaa	aga	tac	ggt	gtg	gaa	cca	528
75	Glu	Leu	Tyr	Asp	Ser	Lys	Lys	Val	Lys	Glu	Arg	Tyr	Gly	Val	Glu	Pro	
76				165						170					175		
78	cat	cag	ata	ccg	gat	ctt	cta	gca	ctg	acg	gga	gac	gag	ata	gac	aac	576
79	His	Gln	Ile	Pro	Asp	Leu	Leu	Ala	Leu	Thr	Gly	Asp	Glu	Ile	Asp	Asn	
80			180					185					190				
82	att	ccc	ggt	gta	acg	gga	ata	ggt	gaa	aag	acc	gct	gta	cag	ctt	ctc	624
83	Ile	Pro	Gly	Val	Thr	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Val	Gln	Leu	Leu	
84		195					200					205					
86	ggc	aag	tac	aga	aat	ctt	gaa	gac	att	ctg	gag	cat	gcc	cgt	gaa	ctc	672
87	Gly	Lys	Tyr	Arg	Asn	Leu	Glu	Asp	Ile	Leu	Glu	His	Ala	Arg	Glu	Leu	
88		210				215					220						
90	ccc	cag	aga	gtg	aga	aag	gct	ctc	ttg	aga	gac	agg	gaa	gtt	gcc	atc	720
91	Pro	Gln	Arg	Val	Arg	Lys	Ala	Leu	Leu	Arg	Asp	Arg	Glu	Val	Ala	Ile	
92	225				230					235				240			
94	ctc	agt	aaa	aaa	ctt	gca	act	ctg	gtg	acg	aac	gca	cct	gtt	gaa	gtg	768
95	Leu	Ser	Lys	Lys	Leu	Ala	Thr	Leu	Val	Thr	Asn	Ala	Pro	Val	Glu	Val	
96			245					250					255				
98	gac	tgg	gaa	gag	atg	aaa	tac	aga	gga	tac	gac	aag	aga	aaa	cta	ctt	816
99	Asp	Trp	Glu	Glu	Met	Lys	Tyr	Arg	Gly	Tyr	Asp	Lys	Arg	Lys	Leu	Leu	
100			260					265				270					
102	ccg	ata	ttg	aaa	gaa	ctg	gag	ttt	gct	tcc	atc	atg	aag	gaa	ctt	caa	864
103	Pro	Ile	Leu	Lys	Glu	Leu	Glu	Phe	Ala	Ser	Ile	Met	Lys	Glu	Leu	Gln	
104		275						280				285					
106	ctg	tac	gaa	gaa	gca	gaa	ccc	acc	gga	tac	gaa	atc	gtg	aag	gat	cat	912
107	Leu	Tyr	Glu	Glu	Ala	Glu	Pro	Thr	Gly	Tyr	Glu	Ile	Val	Lys	Asp	His	
108		290				295					300						
110	aag	acc	ttc	gaa	gat	ctc	atc	gaa	aag	ctg	aag	gag	gtt	cca	tct	ttt	960
111	Lys	Thr	Phe	Glu	Asp	Leu	Ile	Glu	Lys	Leu	Lys	Glu	Val	Pro	Ser	Phe	
112	305				310					315				320			
114	gcc	ctg	gac	ctt	gaa	acg	tcc	tcc	ctt	gac	ccg	ttc	aac	tgt	gag	ata	1008
115	Ala	Leu	Asp	Leu	Glu	Thr	Ser	Ser	Leu	Asp	Pro	Phe	Asn	Cys	Glu	Ile	
116			325					330					335				
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119	Val	Gly	Ile	Ser	Val	Ser	Phe	Lys	Pro	Lys	Thr	Ala	Tyr	Tyr	Ile	Pro	
120			340					345				350					
122	ctt	cat	cac	aga	aac	gcc	cag	aat	ctt	gat	gaa	aca	ctg	gtg	ctg	tcg	1104
123	Leu	His	His	Arg	Asn	Ala	Gln	Asn	Leu	Asp	Glu	Thr	Leu	Val	Leu	Ser	
124			355					360				365					
126	aag	ttg	aaa	gag	atc	ctc	gaa	gac	ccg	tct	tcg	aag	att	gtg	ggt	cag	1152
127	Lys	Leu	Lys	Glu	Ile	Leu	Glu	Asp	Pro	Ser	Ser	Lys	Ile	Val	Gly	Gln	

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132	385 390 395 400			
134	gtt tat ccg cat ttt gac acg atg ata gct gca tat ttg ctg gag cca	1248		
135	Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro			
136	405 410 415			
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139	Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly			
140	420 425 430			
142	tac aaa atg acg tct tat cag gaa ctg atg tcg ttt tcc tca cca ctt	1344		
143	Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu			
144	435 440 445			
146	ttt ggt ttc agc ttt gcg gat gtt ccg gta gac aag gct gcg aac tac	1392		
147	Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr			
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151	Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser			
152	465 470 475 480			
154	atg aag ctc cat gaa gcg gaa ctt gag aac gtc ttc tac agg ata gag	1488		
155	Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu			
156	485 490 495			
158	atg ccg ctt gtg aac gtt ctt gca cgc atg gaa ttg aac ggg gtg tat	1536		
159	Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr			
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163	Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys			
164	515 520 525			
166	ctc gag gaa ctg gcc gaa aaa atc tac cag ata gca gga gag ccc ttc	1632		
167	Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe			
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170	aac atc aat tct cca aaa cag gtt tca aag atc ctt ttt gag aag ctg	1680		
171	Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu			
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174	gga ata aaa ccc cgt gga aaa acg aca aaa gga gcg tac tct acc	1728		
175	Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Ala Tyr Ser Thr			
176	565 570 575			
178	agg ata gag gtg ttg gaa gag ata gcg aat gag cac gag ata gta ccc	1776		
179	Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro			
180	580 585 590			
182	ctc att ctc gag tac aga aag atc cag aaa ctg aaa tcg acc tac ata	1824		
183	Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile			
184	595 600 605			
186	gac acc ctt ccg aaa ctt gtg aac ccg aaa acc gga aga att cat gca	1872		
187	Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala			
188	610 615 620			
190	tct ttc cac cag acg ggt acc gcc act ggc agg ttg agt agc agt gat	1920		
191	Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp			
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198 aga aaa gcg att gtg ccc cag gat cca gac tgg tgg atc gtc agt gcg 2016
199 Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala
200 660 665 670
202 gat tat tcc caa ata gaa ctc aga atc ctc gct cat ctc agt ggt gat 2064
203 Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp
204 675 680 685
206 gag aac ctt gtg aag gcc ttc gag gag ggc atc gat gtg cac acc ttg 2112
207 Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu
208 690 695 700
210 act gcc tcc agg atc tac aac gta aag cca gaa gaa gtg aac gaa gaa 2160
211 Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu
212 705 710 715 720
214 atg cga cgg gtt gga aag atg gtg aac ttc tct ata ata tac ggt gtc 2208
215 Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val
216 725 730 735
218 aca ccg tac ggt ctt tct gtg aga ctt gga ata ccg gtt aaa gaa gca 2256
219 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala
220 740 745 750
222 gaa aag atg att atc agc tat ttc aca ctg tat cca aag gtg cga agc 2304
223 Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser
224 755 760 765
226 tac atc cag cag gtt gtt gca gag gca aaa gag aag ggc tac gtc agg 2352
227 Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg
228 770 775 780
230 act ctc ttt gga aga aaa aga gat att ccc cag ctc atg gca agg gac 2400
231 Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp
232 785 790 795 800
234 aag aac acc cag tcc gaa ggc gaa aga atc gca ata aac acc ccc att 2448
235 Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile
236 805 810 815
238 cag gga acg gcg gca gat ata ata aaa ttg gct atg ata gat ata gac 2496
239 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp
240 820 825 830
242 gag gag ctg aga aaa aga aac atg aaa tcc aga atg atc att cag gtt 2544
243 Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val
244 835 840 845
246 cat gac gaa ctg gtc ttc gag gtt ccc gat gag gaa aaa gaa gaa cta 2592
247 His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu
248 850 855 860
250 gtt gat ctg gtg aag aac aaa atg aca aat gtg gtg aaa ctc tct gtg 2640
251 Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val
252 865 870 875 880
254 cct ctt gag gtt gac ata agc atc gga aaa agc tgg tct tga 2682
255 Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser
256 885 890
259 <210> SEQ ID NO: 2

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/641,319B

DATE: 04/26/2002

TIME: 12:39:38

Input Set : A:\04578--1.txt

Output Set : N:\CRF3\04262002\I641319B.raw

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271 20 25 30
274 Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu
275 35 40 45
278 His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys
279 50 55 60
282 Ala Ala Thr Phe Arg His Lys Leu Leu Glu Ala Tyr Lys Ala Gln Arg
283 65 70 75 80
286 Pro Lys Thr Pro Asp Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg
287 85 90 95
290 Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu
291 100 105 110
294 Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Lys Gly Cys Thr Phe Phe
295 115 120 125
298 Asp Glu Ile Phe Ile Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val
299 130 135 140
302 Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu
303 145 150 155 160
306 Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro
307 165 170 175
310 His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Glu Ile Asp Asn
311 180 185 190
314 Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu
315 195 200 205
318 Gly Lys Tyr Arg Asn Leu Glu Asp Ile Leu Glu His Ala Arg Glu Leu
319 210 215 220
322 Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile
323 225 230 235 240
326 Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val
327 245 250 255
330 Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu
331 260 265 270
334 Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln
335 275 280 285
338 Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His
339 290 295 300
342 Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe
343 305 310 315 320
346 Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile
347 325 330 335
350 Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro
351 340 345 350
354 Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser

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Input Set : A:\04578--1.txt  
Output Set: N:\CRF3\04262002\I641319B.raw

Use of <220> Feature(NEW RULES):

Sequence(s)\_\_\_are missing the <220> Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"  
or "Unknown". Please explain source of genetic material in <220> to <223>  
section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)  
(Sec.1.823 of new Rules)

Seq#: 8, 11, 16, 19, 23, 26, 29, 33, 35, 37, 39

## VERIFICATION SUMMARY

DATE: 04/26/2002

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TIME: 12:39:39

Input Set : A:\04578--1.txt

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